

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:01:59; Search time 32.09 Seconds
(without alignments)
303.844 Million cell updates/sec

Title: US-09-772-103-8
Perfect score: 655
Sequence: 1 MDFQYQIFSILLISAVSILS.....CCQWSSYPLTGGGTKEIK 128

Scoring table: BUOSm62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR:68:
1: Pir1:
2: Pir2:
3: Pir3:
4: Pir4:
A: Residues: 1-130 <KOF>
A: Cross-references: GB:M20834; NID:9196943; PID:AAA38846.1; PID:9196944
C: Superfamily: immunoglobulin V region; immunoglobulin homology
C: Keywords: heterotetramer; immunoglobulin F; 38-113/Domain: immunoglobulin homology <IMM>

Prob. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB ID	Description
1	502	76.6	130	2 A3213	Ig kappa chain pre
2	499	76.2	130	1 JL0079	Ig kappa chain pre
3	498	76.0	235	2 S25058	Ig kappa chain - m
4	491	75.0	140	2 PL0013	Ig kappa chain pre
5	478	73.0	130	2 S0573	Ig kappa chain pre
6	466	71.1	130	2 B32456	Ig kappa chain pre
7	463.5	70.8	107	2 S3264	Ig lambda chain V
8	463.5	70.8	108	2 B49047	Ig kappa chain V
9	463.5	70.8	125	2 S40349	Ig kappa chain V-J
10	455.5	69.5	129	2 S52793	Ig kappa chain V
11	454.5	69.4	107	2 S36269	Ig lambda chain V
12	454.5	69.4	129	2 S40317	Ig kappa chain - h
13	454.5	69.4	129	2 S52789	Ig kappa chain V
14	452.5	69.1	123	2 S40331	Ig kappa chain V
15	452.5	69.1	125	2 S40332	Ig kappa chain - h
16	451.5	68.9	108	2 S19674	Ig kappa chain V-J
17	451.5	68.9	132	2 S40334	Ig kappa chain V
18	447.5	68.3	125	2 S40316	Ig kappa chain - h
19	446	68.1	129	1 KVMSTB	Ig kappa chain pre
20	445.5	68.0	127	2 S40367	Ig kappa chain V-J
21	444.5	67.9	108	1 K1HURY	Ig kappa chain V-I
22	444.5	67.9	108	2 S36277	Ig lambda chain V
23	441.5	67.4	108	1 K1HUBN	Ig kappa chain V-I
24	441.5	67.4	117	2 S463371	Ig kappa chain V-J
25	441.5	67.4	125	2 S40350	Ig kappa chain - h
26	441.5	67.3	132	2 S05268	Ig kappa chain pre
27	439.5	67.1	129	2 S40369	Ig kappa chain - h
28	437.5	66.8	108	2 S36279	Ig lambda chain V
29	436.5	66.6	108	1 K1HORE	Ig kappa chain V-I

RESULT 2

Query Match 76.6%; Score 502; DB 2;
Best Local Similarity 74.6%; pred. No. 1.9e-33;
Matches 97; Conservative 17; Mismatches 14; Indels 2; Gaps 1;

Qy 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Db 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
Db 61 QKPGSSPKWYIYSNLSAGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 120
Qy 119 FGGGTKEIK 128
Db 121 FGTGTKEIK 130

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Db 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
Db 61 QKPGSSPKWYIYSNLSAGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 120
Qy 119 FGGGTKEIK 128
Db 121 FGTGTKEIK 130

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Db 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
Db 61 QKPGSSPKWYIYSNLSAGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 120
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Db 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
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Db 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
Db 61 QKPGSSPKWYIYSNLSAGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 120
Qy 119 FGGGTKEIK 128
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Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
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Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
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Db 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
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Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
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Qy 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Db 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
Db 61 QKPGSSPKWYIYSNLSAGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 120
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Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
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Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
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Db 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
Db 61 QKPGSSPKWYIYSNLSAGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 120
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Qy 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
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Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
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Qy 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
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Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
Db 61 QKPGSSPKWYIYSNLSAGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 120
Qy 119 FGGGTKEIK 128
Db 121 FGTGTKEIK 130

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Best Local Similarity 74.6%; pred. No. 1.9e-33;
Matches 97; Conservative 17; Mismatches 14; Indels 2; Gaps 1;

Qy 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Db 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
Db 61 QKPGSSPKWYIYSNLSAGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 120
Qy 119 FGGGTKEIK 128
Db 121 FGTGTKEIK 130

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Best Local Similarity 74.6%; pred. No. 1.9e-33;
Matches 97; Conservative 17; Mismatches 14; Indels 2; Gaps 1;

Qy 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Db 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
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Db 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
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Qy 119 FGGGTKEIK 128
Db 121 FGTGTKEIK 130

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Best Local Similarity 74.6%; pred. No. 1.9e-33;
Matches 97; Conservative 17; Mismatches 14; Indels 2; Gaps 1;

Qy 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Db 1 MDFOYQIFSILLISAVSILS25058S25058S25058S25058S25058
Qy 59 QKPGKAPKULLYDPSNL1AGVPSRSFSSGGTDYTLTSSLQPEDFATYYCOCWSSYPLT 118
Db 61 QKPGSSPKWY

A; Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation	QY	61	PGKAPKLLIYDTSNLASGVPSRFSGSGSGTDTLTISSLOPEDATYYCQWSSYPLTFFG	120
R; Milstein, C.; Evans, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.	Db	61	SGTSPKRWYDTSKLASGVPSRFSGSGSGTDTLTISSMBAEDAATYYCQWSSYPLTFFG	120
Eur. J. Immunol. 22, 1627-1634, 1992				
A; Title: Non-random features of the repertoire expressed by the members of one V kappa				
A; Reference number: A49044; MUID:32289826				
A; Accession: A49044				
A; Molecule type: DNA				
A; Residues: 1-25 <MIL>				
A; Cross-references: GB:S37663; NID:9250214; PIDN:AAB22331.1; PID:g20217				
A; Note: sequence extracted from NCBI backbone (NCBIN:106802, NCBIPI:106809)				
A; Accession: Ba2044				
A; Molecule type: DNA				
A; Residues: 14-116 <MIL2>				
A; Cross-references: GB:S37664; NID:9250215; PIDN:AAB22332.1; PID:g250218				
A; Experimental source: B4B/c germ-line				
A; Note: sequences extracted from NCBI backbone; partial nucleotide sequences of 13 addit				
A; Note: sequences extracted from NCBI backbone (NCBIN:106807, NCBIPI:106822)				
A; Genetics:				
A; Gene: V(kappa)0x1				
A; Introns: 17/1				
A; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap				
A; disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 18				
C; Superfamily: immunoglobulin V region; immunoglobulin homology				
C; Keywords: heterotetramer; immunoglobulin				
F; 1-22/Domain: signal sequence #status predicted <MAT>				
F; 23-130/Product: Ig kappa chain V region (6F6) #status predicted <MAT>				
F; 38-111/Domain: immunoglobulin homology <IMM>				
F; 45-109/Disulfide bonds: #status predicted				
Query Match	76.2%	Score 499;	DB 1;	Length 130;
Best Local Similarity	74.2%	Pred. No. 3_3e-33;	Indels 0;	Gaps 0;
Matches 95; Conservative 16; Mismatches 17;				
Query Match	76.2%	Score 499;	DB 1;	Length 130;
Best Local Similarity	74.2%	Pred. No. 3_3e-33;	Indels 0;	Gaps 0;
Matches 95; Conservative 16; Mismatches 17;				
QY	1	MDFQVQIFSFLLISAVIILSQRDIQMTQPSLSSAISYCDRTTCSATSSITIYMSWYQK	60	
Db	1	MDFQVQIFSFLLISAVIILSQRDIQMTQPSLSSAISYCDRTTCSATSSITIYMSWYQK	60	
QY	61	PGKAPKLLIYDTSNLASGVPSRFSGSGSGTDTLTISSLOPEDATYYCQWSSYPLTFFG	120	
Db	61	SGTSPKRWYDTSKLASGVPSRFSGSGSGTDTLTISSMBAEDAATYYCQWSSYPLTFFG	120	
QY	121	GGTKVEIK 128		
Db	121	GGTKVEIK 128		
RESULT	3			
Q58				
C; Species: Mus musculus (house mouse)				
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000				
R; Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.				
A; Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific				
A; Reference number: S25057				
A; Status: preliminary				
A; Molecule type: mRNA				
A; Residues: 1-235 <F1>				
A; Cross-references: EMBL:X67211; NID:954828; PIDN:CAA47650.1; PID:954829				
C; Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>				
F; 38-111/Domain: immunoglobulin homology <IMM>				
Query Match	76.0%	Score 498;	DB 2;	Length 235;
Best Local Similarity	74.2%	Pred. No. 7e-33;	Indels 0;	Gaps 0;
Matches 95; Conservative 16; Mismatches 17;				
QY	1	MDFQVQIFSFLLISAVIILSQRDIQMTQPSLSSAISYCDRTTCSATSSITIYMSWYQK	60	
Db	1	SGTSPKRWYDTSKLASGVPSRFSGSGSGTDTLTISSMBAEDAATYYCQWSSYPLTFFG	120	

Query Match 73.0%; Score 478; DB 2; Length 130;
 Best Local Similarity 70.8%; Pred. No. 1.6e-31;
 Matches 92; Conservative 22; Mismatches 14; Indels 2; Gaps 1;
 C:Species: Mus musculus (house mouse)
 C:Accession: B32456
 R:J.Dombroski-Kurtzman, M.A.; Johnson, L.S.; Riordan, G.S.; Bedzyk, W.D.; Voss Jr., E.W.
 A:Title: Variable region primary structures of a high affinity anti-fluorescein immunog
 A:Reference number: A32456; MUID:89174706
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-130 <DOM>
 A:Cross-references: GB:T04610; NID:9556313; PIDN:AA50296..1; PID:9556314
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin F; 38-113/Domain: immunoglobulin homology <IMM>

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 463.5; DB 2; Length 107;
 Best Local Similarity 83.2%; Pred. No. 1.8e-30;
 Matches 89; Conservative 11; Mismatches 6; Indels 1; Gaps 1;
 C:Species: Homo sapiens (man)
 C:Accession: B49047
 R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
 Eur. J. Immunol. 22, 2231-2236, 1992
 A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocyt
 A:Reference number: A49047; MUID:92387224
 A:Accession: B49047
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-108 <VIC>
 A:Experimental source: thymic B lymphocytes
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 463.5; DB 2; Length 108;

Best Local Similarity 86.0%; Pred. No. 1.9e-30;
 Matches 92; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 1 MDFOYQIFSFLLISAVSILSRGDIQMTOSSPLSASVGDRVTITCSATSSIT--YMSWYQ 58
 Db 1 MDFQYQIFSFLLISAVSILSRGDIQMTOSSPLSASVGDRVTITCSATSSIT--YMSWYQ 58

QY 59 QKPGKAPKLITYDTSNLASGVPSRFSSGSIDYDTLTISSLOPEDFATYYCQWSSYPLT 118
 Db 61 QKSGASPALKWYCTNSNLASGVPARFSSGSGTSYSLTISSEDAATYYCQYHSDPLT 120

QY 119 FGCGTKVEIK 128
 Db 121 FGAGTKLELK 130

RESULT 8

B49047

Ig kappa chain V region (monoclonal striational autoantibody STRAB SA-1A) - human (fr

C:Species: Homo sapiens (man)

C:Accession: B1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000

R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.

Eur. J. Immunol. 22, 2231-2236, 1992

A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocyt

A:Reference number: A49047; MUID:92387224

A:Accession: B49047

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-108 <VIC>

A:Experimental source: thymic B lymphocytes

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 463.5; DB 2; Length 108;

Best Local Similarity 86.0%; Pred. No. 1.9e-30;
 Matches 92; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 23 DQMTQSPSSLSASVGDRVTITCSATSSIT-YMSWYQKPGKAPKLITYDTSNLASGVPS 81
 Db 1 EIVLQSPSSLSASVGDRVTITCSATSSIT-YMSWYQKPGKAPKLITYAASSLQSGVPS 60

QY 82 RFSGSGTDTYDFTLTISSEDAATYYCQWSSYPLT 128
 Db 61 RFSGSGTDTYDFTLTISSEDAATYYCQWSSYPLT 107

RESULT 9

S40349

Ig kappa chain V-J region

- human

C:Species: Homo sapiens (man)

C:Accession: S40312; MUID:9408891

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312

A:Accession: S40349

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-125 <KLE>

A:Cross-references: EMBL:Z18845; NID:9441386; PIDN:AA511227; PID:9441387

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin F; 33-107/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 463.5; DB 2; Length 125;

Best Local Similarity 81.8%; Pred. No. 2.1e-30;
 Matches 90; Conservative 11; Mismatches 8; Indels 1; Gaps 1;

C:Keywords: heterotetramer; immunoglobulin

C:Keywords: heterotetramer; immunoglobulin

C:Keywords: heterotetramer; immunoglobulin

Qy	82	REFSGSGSTDTYLTISLQEDFATYYCQWSYSSPFLFGGTKEYIK 128	
Db	61	REFSGSGSTDTFLTISLQEDFATYYCQQTTSFLTFGGTKEYIK 107	
	RESULT 12		
SA0317		Ig kappa chain - human	
C:Species: Homo sapiens (man)			
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_cha			
C:Accession: S40317			
R:Klein, R.; Jaenichen, R.; Zachau, H.G.			
Eur. J. Immunol. 23, 3218-3271, 1993			
A:Title: Expressed human immunoglobulin chi genes and their homologues			
A:Reference number: S40312; PMID:94080891			
A:Accession: S40317			
A:Status: Preliminary; translation not shown			
A:Molecule type: mRNA			
A:Residues: 1-129 <RLE>			
A:Cross-references: EMBL:X72427; PIDN:CAA51095.1			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
C:Keywords: heterotramer; immunoglobulin			
F:37-111/Domain: immunoglobulin homology <IMM>			
	Query Match 69.4%; Score 454.5; DB 2; Length 121		
Best Local Similarity 81.8%; Pred. No. 1.1e-29;			
Matches 90; Conservative 7; Mismatches 12; Indels 1			
SA0317			
Query 20 SRGDIQMTQSSSLASAVGDRVTITCSATSSI-TYMSWYQOKPGKAPKLL			
Db 19 ARCDIQMTQSSSLSLSGDRVTITCSATSSI-TYMSWYQOKPGKAPKFL			
Qy 79 VPSRFSGSGSTDTFLTISLQEDFATYYCQWSYSSPFLFGGTKEYIK			
Db 79 VPSRFSGSGSTDTFLTISLQEDFATYYCQQTTSFLTFGGTKEYIK			
	RESULT 13		
SA2289		Ig kappa chain V region - human (fragment)	
C:Species: Homo sapiens (man)			
C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_cha			
C:Accession: S52789			
R:Rocca, A.; Khamlich, A.A.; Touchard, G.; Mougenot, B.; Ro			
submitted to the EMBL Data Library, March 1995			
A:Description: Light chain V region gene usage restriction analysis			
A:Reference number: S52789			
A:Accession: S52789			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-129 <ROC>			
A:Cross-references: EMBL:X85995; PIDN:CAA59987			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
C:Keywords: heterotrimer; immunoglobulin			
F:38-112/Domain: immunoglobulin homology <IMM>			
	Query Match 69.4%; Score 454.5; DB 2; Length 121		
Best Local Similarity 71.0%; Pred. No. 1.1e-29;			
Matches 93; Conservative 15; Mismatches 18; Indels 1			
SA2289			
Query 1 MDFQV-QIFSEFLISASVILSRGDIQMTQSSSLASAVGDRVTITCSA			
Db 1 MDMRVPAQLGLLILWLSG-ARCDIQMTQSSSLASAVGDRVTITCSAQ			
Qy 58 QKPKQKPKLIYDTSNLASGVPSPFSGSGSTDTFLTISLQEDFAT			
Db 59 QKPKQKPKLIYDTSNLASGVPSPFSGSGSTDTFLTISLQEDFAT			
Qy 118 TFGGTKEYIK 128			

Db 119 TFGGGTKVEIK 129

RESULT 14

S40331

Ig kappa chain - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40331

R:Klein, R.; Jaenichen, R.; Zachau, H. G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891

A;Accession: S40331

A;Status: Preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-123 <KLE>

A;Cross-references: EMBL:X72441; PID:9441350; PID:CAA51109.1; PID:9441351

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 452.5; DB 2; Length 123;
 Best Local Similarity 82.7%; Pred. No. 1.6e-29; Mismatches 7; Indels 1; Gaps 1;
 Matches 91; Conservative 7; MisMatches 11;

QY 20 SRDQMTQSPSSLSASVGRVTITCSATSSI-TYMSWYQOKPGKAPLILYDTNSNLASG 78
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||:
 DB 14 ARCDIQMTQSPSSLSASVGRVTITCSATSSI-TYMSWYQOKPGKAPLILYDTNSNLASG 73
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||:
 QY 79 VPSRFSGSGTGTDTITLSSLOPEDATYYCQWQSSYPLTFCGGTKEIK 128
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 DB 74 VPSRFSGSGTGTDTITLSSLOPEDATYYCQWQSSYPLTFCGGTKEIK 123
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 QY 80 VPSRFSGSGTGTDTITLSSLOPEDATYYCQWQSSYPLTFCGGTKEIK 123

RESULT 15

S40333

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40333

R:Klein, R.; Jaenichen, R.; Zachau, H. G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891

A;Accession: S40333

A;Status: Preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-125 <KLE>

A;Cross-references: EMBL:X72443; PID:9441354; PID:CAA51111.1; PID:9441355

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-108/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 452.5; DB 2; Length 125;
 Best Local Similarity 81.3%; Pred. No. 1.6e-29; Mismatches 12; Indels 1; Gaps 1;
 Matches 87; Conservative 7; MisMatches 11;

QY 23 DIQMTQSPSSLSASVGRVTITCSATSSI-TYMSWYQOKPGKAPLILYDTNSNLASGPS 81
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||:
 DB 19 DIQMTQSPSSLSASVGRVTITCSATSSI-TYMSWYQOKPGKAPLILYDTNSNLASGPS 78
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 QY 82 RFSGSGSGTGTDTITLSSLOPEDATYYCQWQSSYPLTFCGGTKEIK 128
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 DB 79 RFSGSGSGTGTDTITLSSLOPEDATYYCQWQSSYPLTFCGGTKEIK 125

